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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/966,264

DATE: 10/16/2001
TIME: 15:04:40

Input Set : A:\Barber Sequence Listing.txt
Output Set: N:\CRF3\10162001\I966264.raw

3 <110> APPLICANT: Barber, Elizabeth K
5 <120> TITLE OF INVENTION: Gene Expression Control Element DNA
7 <130> FILE REFERENCE: 896034605001
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/966,264
C--> 9 <141> CURRENT FILING DATE: 2001-09-28
9 <150> PRIOR APPLICATION NUMBER: US 60/237,079
10 <151> PRIOR FILING DATE: 2000-09-30
12 <160> NUMBER OF SEQ ID NOS: 33
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 137
18 <212> TYPE: DNA
19 <213> ORGANISM: human
21 <220> FEATURE:
22 <221> NAME/KEY: exon
23 <222> LOCATION: (3)..(137)
24 <223> OTHER INFORMATION:
27 <220> FEATURE:
28 <221> NAME/KEY: polyA_site
29 <222> LOCATION: (130)..(135)
30 <223> OTHER INFORMATION:
33 <400> SEQUENCE: 1
34 at tat aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg 47
35 Tyr Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu
36 1 5 10
38 tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95
39 Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys
40 15 20 25
42 ggt aga aat agc atg aga agc cgt gtt tga tgt taa tta att 137
43 Gly Arg Asn Ser Met Arg Ser Arg Val Cys Leu Ile
44 30 35 40
47 <210> SEQ ID NO: 2
48 <211> LENGTH: 996
49 <212> TYPE: DNA
50 <213> ORGANISM: human
52 <220> FEATURE:
53 <221> NAME/KEY: exon
54 <222> LOCATION: (1)..(996)
55 <223> OTHER INFORMATION:
58 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
60 <222> LOCATION: (710)..(996)
61 <223> OTHER INFORMATION: Nucleotides 710-996 are homologous to a portion of human
dystrophin
62 in DNA in the region of exon 79 except that nucleotides 860-996 a
63 re inverted in comparison to the orientation of the same sequence
64 in the dystrophin DNA
67 <400> SEQUENCE: 2

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68	gtg	gtt	tga	ttg	ata	gta	aaa	aaa	atg	ttc	gtt	aat	aca	agt	aga	gag	48
69	Val	Val		Leu	Ile	Val	Lys	Lys	Met	Phe	Val	Asn	Thr	Ser	Arg	Glu	
70	1					5					10					15	
72	taa	gta	atc	aat	caa	tca	ctc	ata	gcc	aag	gtg	gaa	aag	atg	tat	ccc	96
73																	
73	Val	Ile	Asn	Gln	Ser	Leu	Ile	Ala	Lys	Val	Glu	Lys	Met	Tyr	Pro		
74											20		25			30	
76	atc	atg	gaa	tat	tcc	tgt	tct	gat	aga	aat	ctt	gtg	ctt	atc	tat	gga	144
77	Ile	Met	Glu	Tyr	Ser	Cys	Ser	Asp	Arg	Asn	Leu	Val	Leu	Ile	Tyr	Gly	
78											35		40			45	
80	att	ctt	ttg	ata	tat	att	tac	att	ggg	aac	ctg	aat	gta	gct	tga	cat	192
81	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu	Asn	Val	Ala		His	
82											50		55			60	
84	ttt	tcc	atg	taa	aca	cca	gta	gcc	tga	tcc	aat	aag	ctg	ata	cta		240
85	Phe	Ser	Met		Thr	Pro	Val	Ala		Ser	Asn	Ile	Lys	Leu	Ile	Leu	
86											65		70			75	
88	aca	aac	aac	gtg	taa	tgg	ctt	cat	taa	taa	ggc	ttt	gct	tct	tcc	tgg	288
89	Thr	Asn	Asn	Val		Trp	Leu	His			Gly	Phe	Ala	Ser	Ser	Trp	
90											80		85				
92	aaa	ctg	gtg	aaa	aat	caa	acc	ttg	ttg	tgt	aca	ccc	tcg	atg	cag	ctt	336
93	Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	
94											90		95			100	
96	ctg	tgt	tgt	ctt	cac	cca	gaa	atg	ggg	aat	gat	ttc	cca	aat	ggc	aaa	384
97	Leu	Cys	Cys	Leu	His	Pro	Glu	Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys	
98	105						110				115					120	
100	gaa	aca	gag	tga	tgc	tat	cta	tct	gca	cct	ttt	gta	aag	tct	gtc	ttt	432
101	Glu	Thr	Glu		Cys	Tyr	Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe	
102							125				130					135	
104	ctt	tct	ctt	tgt	ttt	cca	gga	cac	aat	gta	gga	agt	ctt	ttc	cac	atg	480
105	Leu	Ser	Leu	Cys	Phe	Pro	Gly	His	Asn	Val	Gly	Ser	Leu	Phe	His	Met	
106							140			145					150		
108	gca	gat	gat	ttg	ggc	aga	gca	ttg	gag	tcc	tta	gta	tca	gtc	atg	aca	528
109	Ala	Asp	Asp	Leu	Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr	
110							155			160					165		
112	gat	gaa	gaa	gga	gca	gaa	taa	atg	ttt	tac	aac	tcc	tga	tcc	ccg	cat	576
113	Asp	Glu	Glu	Gly	Ala	Glu		Met	Phe	Tyr	Asn	Ser		Phe	Pro	His	
114							170			175					180		
116	ggt	ttt	tat	aat	att	att	cat	aca	aca	aag	agg	att	aga	cag	taa	gag	624
117	Gly	Phe	Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln		Glu	Phe	
118							185			190					195		
120	aca	aga	aat	aaa	tct	ata	ttt	ttg	tga	agg	gtt	gtt	gtt	tta	tac	tgt	672
121	Thr	Arg	Asn	Lys	Ser	Ile	Phe	Leu		Arg	Val	Val	Val	Leu	Tyr	Cys	
122							200			205					210		
124	aga	ttt	cag	tag	ttt	cta	agt	ctg	tta	ttt	tgt	taa	caa	tgg	cag		720
125	Arg	Phe	Gln		Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys		Gln	Trp	Gln	
126							215			220					225		
128	gtt	tta	cac	gtc	tat	gca	att	gta	caa	aaa	agt	tat	aag	aaa	act	aca	768
129	Val	Leu	His	Val	Tyr	Ala	Ile	Val	Gln	Lys	Ser	Tyr	Lys	Lys	Thr	Thr	
130							230			235					240		
132	tgt	aaa	atc	ttg	ata	gct	aaa	taa	ctt	gcc	att	tct	tta	tat	gga	acg	816

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133	Cys Lys Ile Leu Ile Ala Lys	Leu Ala Ile Ser Leu Tyr Gly Thr	
134	245	250	255
136	cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat		864
137	His Phe Gly Leu Phe Lys Asn Leu	Gln Leu	Arg Lys Asn Tyr
138	260	265	270
140	aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act		912
141	Lys Gly Lys Arg Lys	Arg Asn Gly Gln Val Val Lys Leu	Thr
142	275	280	
144	cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga		960
145	Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys	Gly Arg	
146	285	290	295
148	aat agc atg aga agc cgt gtt tga tgt taa tta att		996
149	Asn Ser Met Arg Ser Arg Val	Cys	Leu Ile
150	300	305	
153	<210> SEQ ID NO: 3		
154	<211> LENGTH: 13		
155	<212> TYPE: PRT		
156	<213> ORGANISM: human		
158	<400> SEQUENCE: 3		
160	Met Tyr Pro Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn		
161	1	5	10
164	<210> SEQ ID NO: 4		
165	<211> LENGTH: 13		
166	<212> TYPE: PRT		
167	<213> ORGANISM: human		
169	<400> SEQUENCE: 4		
171	Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala Asp Thr Met		
172	1	5	10
175	<210> SEQ ID NO: 5		
176	<211> LENGTH: 18		
177	<212> TYPE: PRT		
178	<213> ORGANISM: human		
180	<400> SEQUENCE: 5		
182	Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp		
183	1	5	10
186	Glu Glu		
190	<210> SEQ ID NO: 6		
191	<211> LENGTH: 10		
192	<212> TYPE: DNA		
193	<213> ORGANISM: human		
195	<400> SEQUENCE: 6		
196	acttacctgt		10
199	<210> SEQ ID NO: 7		
200	<211> LENGTH: 22		
201	<212> TYPE: DNA		
202	<213> ORGANISM: human		
204	<400> SEQUENCE: 7		
205	ttataaagaa agaattataa ag		22
208	<210> SEQ ID NO: 8		

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Input Set : A:\Barber Sequence Listing.txt
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209 <211> LENGTH: 42
210 <212> TYPE: DNA
211 <213> ORGANISM: human
213 <400> SEQUENCE: 8
214 ccttggctat gagtgattga ttgattactt actctctact tg 42
217 <210> SEQ ID NO: 9
218 <211> LENGTH: 20
219 <212> TYPE: DNA
220 <213> ORGANISM: human
222 <400> SEQUENCE: 9
223 gattgatagt aaaaaaaaaatg 20
226 <210> SEQ ID NO: 10
227 <211> LENGTH: 21
228 <212> TYPE: DNA
229 <213> ORGANISM: human
231 <400> SEQUENCE: 10
232 caatggcagg ttttacacgt c 21
235 <210> SEQ ID NO: 11
236 <211> LENGTH: 20
237 <212> TYPE: DNA
238 <213> ORGANISM: human
240 <400> SEQUENCE: 11
241 ggaaaagact tccacattgt 20
244 <210> SEQ ID NO: 12
245 <211> LENGTH: 22
246 <212> TYPE: DNA
247 <213> ORGANISM: human
249 <400> SEQUENCE: 12
250 ctttttcctt tataattctt tc 22
253 <210> SEQ ID NO: 13
254 <211> LENGTH: 22
255 <212> TYPE: DNA
256 <213> ORGANISM: human
258 <400> SEQUENCE: 13
259 catcaaacac ggcttctcat gc 22
262 <210> SEQ ID NO: 14
263 <211> LENGTH: 9
264 <212> TYPE: PRT
265 <213> ORGANISM: human
267 <220> FEATURE:
268 <221> NAME/KEY: MISC_FEATURE
269 <222> LOCATION: (1)..(3)
270 <223> OTHER INFORMATION: histone methylation site
273 <220> FEATURE:
274 <221> NAME/KEY: MISC_FEATURE
275 <222> LOCATION: (7)..(9)
276 <223> OTHER INFORMATION: histone methylation site
279 <400> SEQUENCE: 14
281 Arg Lys Asn Tyr Lys Gly Lys Arg Lys

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Input Set : A:\Barber Sequence Listing.txt
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282 1	5	
285 <210> SEQ ID NO: 15		
286 <211> LENGTH: 18		
287 <212> TYPE: DNA		
288 <213> ORGANISM: human		
290 <400> SEQUENCE: 15		
291 gttcggttaat acaagtag	18	
294 <210> SEQ ID NO: 16		
295 <211> LENGTH: 18		
296 <212> TYPE: DNA		
297 <213> ORGANISM: human		
299 <400> SEQUENCE: 16		
300 gccaagggtgg aaaagatg	18	
303 <210> SEQ ID NO: 17		
304 <211> LENGTH: 18		
305 <212> TYPE: DNA		
306 <213> ORGANISM: human		
308 <400> SEQUENCE: 17		
309 ccagtagcct gatccaac	18	
312 <210> SEQ ID NO: 18		
313 <211> LENGTH: 15		
314 <212> TYPE: DNA		
315 <213> ORGANISM: human		
317 <400> SEQUENCE: 18		
318 ggcttcattt ataag	15	
321 <210> SEQ ID NO: 19		
322 <211> LENGTH: 17		
323 <212> TYPE: DNA		
324 <213> ORGANISM: human		
326 <400> SEQUENCE: 19		
327 ggc当地aaaa cagatgt	17	
330 <210> SEQ ID NO: 20		
331 <211> LENGTH: 17		
332 <212> TYPE: DNA		
333 <213> ORGANISM: human		
335 <400> SEQUENCE: 20		
336 caggacacaa tgttagga	17	
339 <210> SEQ ID NO: 21		
340 <211> LENGTH: 23		
341 <212> TYPE: DNA		
342 <213> ORGANISM: human		
344 <400> SEQUENCE: 21		
345 gttataaaaga aagaattata aag	23	
348 <210> SEQ ID NO: 22		
349 <211> LENGTH: 18		
350 <212> TYPE: DNA		
351 <213> ORGANISM: human		
353 <400> SEQUENCE: 22		
354 gaaaataacg caatggac	18	

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/966,264

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Input Set : A:\Barber Sequence Listing.txt
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date